

A circular stamp from the Office of Intellectual Property (OIPE). The text "OIPE" is at the top, "JC178" is at the top right, "MAR 14 2002" is in the center, and "PATENT &amp; TRADEMARK OFFICE" is at the bottom. The stamp is slightly tilted.

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ttc | tgg | ccg | gat | gat | acc | atc | ttc | act | gtt | acc | gaa | tat | aag | ttt | gac | 240 |
| Phe | Trp | Pro | Asp | Asp | Thr | Ile | Phe | Thr | Val | Thr | Glu | Tyr | Lys | Phe | Asp |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |

|   |     |
|---|-----|
| att cta cag gca cgt atg cgt gaa ttg gcc tac ttg aac aaa ggt atc | 288 |
| Ile Leu Gln Ala Arg Met Arg Glu Leu Ala Tyr Leu Asn Lys Gly Ile |     |
| 85 90 95  |     |
| acc att tca ctg acc gac cgc cgg atc aaa gaa gaa gat ggc agc ttc | 336 |
| Thr Ile Ser Leu Thr Asp Arg Arg Ile Lys Glu Glu Asp Gly Ser Phe |     |
| 100 105 110   |     |
| aag aaa gaa ata ttc cat tcg gac gaa gga gtg aaa gag ttt gta cgt | 384 |
| Lys Lys Glu Ile Phe His Ser Asp Glu Gly Val Lys Glu Phe Val Arg |     |
| 115 120 125   |     |
| ttc ctg aac cgt aac aac gaa gcg ctg att aat gat gtc att tat ctg | 432 |
| Phe Leu Asn Arg Asn Asn Glu Ala Leu Ile Asn Asp Val Ile Tyr Leu |     |
| 130 135 140   |     |
| aat acc gaa aaa aac aat acc ccc att gaa tgt gcc atc atg tac aat | 480 |
| Asn Thr Glu Lys Asn Asn Thr Pro Ile Glu Cys Ala Ile Met Tyr Asn |     |
| 145 150 155 160   |     |
| aca ggc tat cgt gaa agc ctg cat tcg tat gta aac aat atc aat aca | 528 |
| Thr Gly Tyr Arg Glu Ser Leu His Ser Tyr Val Asn Asn Ile Asn Thr |     |
| 165 170 175   |     |
| ata gaa ggc ggt aca cac gag gcc ggt ttc cgc agc gca tta acc cgt | 576 |
| Ile Glu Gly Gly Thr His Glu Ala Gly Phe Arg Ser Ala Leu Thr Arg |     |
| 180 185 190   |     |
| gta ctg aag aaa tat gcg gaa gat acc aaa gca ctg gaa aaa gca aaa | 624 |
| Val Leu Lys Lys Tyr Ala Glu Asp Thr Lys Ala Leu Glu Lys Ala Lys |     |
| 195 200 205   |     |
| gtc gag att tcg gga gag gac ttc cgc gaa ggc ttg att gcc gtc att | 672 |
| Val Glu Ile Ser Gly Glu Asp Phe Arg Glu Gly Leu Ile Ala Val Ile |     |
| 210 215 220   |     |
| tca gtg aaa gta gcc gag ccg cag ttc gaa gga cag acc aag acc aag | 720 |
| Ser Val Lys Val Ala Glu Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys |     |
| 225 230 235 240   |     |
| ctg ggc aac agc gaa gtg agt ggt gcc gtg aac caa gct gta ggc gaa | 768 |
| Leu Gly Asn Ser Glu Val Ser Gly Ala Val Asn Gln Ala Val Gly Glu |     |
| 245 250 255   |     |
| gcg ctt aca tat tat ctg gaa gaa cat ccg aaa gaa gca aaa cag att | 816 |
| Ala Leu Thr Tyr Tyr Leu Glu Glu His Pro Lys Glu Ala Lys Gln Ile |     |
| 260 265 270   |     |
| gtt gac aaa gtg atc ctg gct gca aca gcg cgt atc gcc gca cgc aag | 864 |
| Val Asp Lys Val Ile Leu Ala Ala Thr Ala Arg Ile Ala Ala Arg Lys |     |
| 275 280 285   |     |
| gca cgt gaa tct gtt caa aga aag agt ccg atg ggc ggt ggc gga ctg | 912 |
| Ala Arg Glu Ser Val Gln Arg Lys Ser Pro Met Gly Gly Gly Gly Leu |     |
| 290 295 300   |     |
| ccg ggc aaa ctg gcc gac tgc tcg agc cgt aat ccg gag gaa tgt gaa | 960 |

Pro Gly Lys Leu Ala Asp Cys Ser Ser Arg Asn Pro Glu Glu Cys Glu  
 305 310 315 320

cta ttc ctg gtc gag ggt gac tcg gca ggt ggt tct gcc aag caa gga 1008  
 Leu Phe Leu Val Glu Gly Asp Ser Ala Gly Gly Ser Ala Lys Gln Gly  
 325 330 335

cgt agc cgt gcc ttc cag gca att cta cct ttg agg ggt aaa atc ctg 1056  
 Arg Ser Arg Ala Phe Gln Ala Ile Leu Pro Leu Arg Gly Lys Ile Leu  
 340 345 350

aat gtg gaa aaa gcg atg tgg cac aag gct ttt gaa agc gat gag gtc 1104  
 Asn Val Glu Lys Ala Met Trp His Lys Ala Phe Glu Ser Asp Glu Val  
 355 360 365

aat aat atc atc acc gcc ctg ggt gtc cgt ttc ggt gtg gac gga aat 1152  
 Asn Asn Ile Ile Thr Ala Leu Gly Val Arg Phe Gly Val Asp Gly Asn  
 370 375 380

gat gac agc aaa aaa gcg aac atc gac aag ctg cgt tat cac aaa gtg 1200  
 Asp Asp Ser Lys Lys Ala Asn Ile Asp Lys Leu Arg Tyr His Lys Val  
 385 390 395 400

gtg atc atg acc  
 Val Ile Met Thr

<210> 2

<211> 404

<212> PRT

<213> Bacteroides vulgatus

<400> 2

Asp Lys Gly Ser Tyr Lys Val Ser Gly Gly Leu His Gly Val Gly Val  
 1 5 10 15  
 Ser Cys Val Asn Ala Leu Ser Thr His Met Thr Thr Gln Val Phe Arg  
 20 25 30  
 Gly Gly Lys Ile Tyr Gln Gln Glu Tyr Ser Cys Gly His Pro Leu Tyr  
 35 40 45  
 Ser Val Lys Glu Val Gly Thr Ala Asp Ile Thr Gly Thr Lys Gln Thr  
 50 55 60  
 Phe Trp Pro Asp Asp Thr Ile Phe Thr Val Thr Glu Tyr Lys Phe Asp  
 65 70 75 80  
 Ile Leu Gln Ala Arg Met Arg Glu Leu Ala Tyr Leu Asn Lys Gly Ile  
 85 90 95  
 Thr Ile Ser Leu Thr Asp Arg Arg Ile Lys Glu Glu Asp Gly Ser Phe  
 100 105 110  
 Lys Lys Glu Ile Phe His Ser Asp Glu Gly Val Lys Glu Phe Val Arg  
 115 120 125  
 Phe Leu Asn Arg Asn Asn Glu Ala Leu Ile Asn Asp Val Ile Tyr Leu  
 130 135 140  
 Asn Thr Glu Lys Asn Asn Thr Pro Ile Glu Cys Ala Ile Met Tyr Asn  
 145 150 155 160  
 Thr Gly Tyr Arg Glu Ser Leu His Ser Tyr Val Asn Asn Ile Asn Thr  
 165 170 175  
 Ile Glu Gly Gly Thr His Glu Ala Gly Phe Arg Ser Ala Leu Thr Arg  
 180 185 190

Val Leu Lys Lys Tyr Ala Glu Asp Thr Lys Ala Leu Glu Lys Ala Lys  
 195 200 205  
 Val Glu Ile Ser Gly Glu Asp Phe Arg Glu Gly Leu Ile Ala Val Ile  
 210 215 220  
 Ser Val Lys Val Ala Glu Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys  
 225 230 235 240  
 Leu Gly Asn Ser Glu Val Ser Gly Ala Val Asn Gln Ala Val Gly Glu  
 245 250 255  
 Ala Leu Thr Tyr Tyr Leu Glu Glu His Pro Lys Glu Ala Lys Gln Ile  
 260 265 270  
 Val Asp Lys Val Ile Leu Ala Ala Thr Ala Arg Ile Ala Ala Arg Lys  
 275 280 285  
 Ala Arg Glu Ser Val Gln Arg Lys Ser Pro Met Gly Gly Gly Gly Leu  
 290 295 300  
 Pro Gly Lys Leu Ala Asp Cys Ser Ser Arg Asn Pro Glu Glu Cys Glu  
 305 310 315 320  
 Leu Phe Leu Val Glu Gly Asp Ser Ala Gly Gly Ser Ala Lys Gln Gly  
 325 330 335  
 Arg Ser Arg Ala Phe Gln Ala Ile Leu Pro Leu Arg Gly Lys Ile Leu  
 340 345 350  
 Asn Val Glu Lys Ala Met Trp His Lys Ala Phe Glu Ser Asp Glu Val  
 355 360 365  
 Asn Asn Ile Ile Thr Ala Leu Gly Val Arg Phe Gly Val Asp Gly Asn  
 370 375 380  
 Asp Asp Ser Lys Lys Ala Asn Ile Asp Lys Leu Arg Tyr His Lys Val  
 385 390 395 400  
 Val Ile Met Thr

<210> 3  
 <211> 1263  
 <212> DNA  
 <213> Mycobacterium simiae

<220>  
 <221> CDS  
 <222> (1)...(1263)

<400> 3  
 ggg gag aac agt ggc tac acc gtc agc ggc ggg ttg cac ggg gtc gga 48  
 Gly Glu Asn Ser Gly Tyr Thr Val Ser Gly Gly Leu His Gly Val Gly  
 1 5 10 15  
 gtg tcg gtg gtc aac gcc ctg tcc acc cgc ctg gaa gtc aac gtc aag 96  
 Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asn Val Lys  
 20 25 30  
 cgt gac ggc tat gag tgg ttc cag tac tac gac cgg gcg gtg ccc ggc 144  
 Arg Asp Gly Tyr Glu Trp Phe Gln Tyr Tyr Asp Arg Ala Val Pro Gly  
 35 40 45  
 acc ctc aag caa ggc gag gcg acc aag aag acc ggc acc acg atc cgg 192  
 Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg  
 50 55 60  
 ttc tgg gcc gat cct gag atc ttc gaa acc acc cag tac gac ttc gag 240  
 Phe Trp Ala Asp Pro Glu Ile Phe Glu Thr Thr Gln Tyr Asp Phe Glu

| 65  | 70  | 75  | 80  |     |
|---|-----|-----|-----|-----|
| acg gtg gcg cgc cgg ttg cag gaa atg gcg ttc ctc aac aag ggc ctg |     |     |     | 288 |
| Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu | 85  | 90  | 95  |     |
| acc atc aac ctc acc gac gaa cgt gtc gag cag gac gag gtg gtc gat |     |     |     | 336 |
| Thr Ile Asn Leu Thr Asp Glu Arg Val Glu Gln Asp Glu Val Val Asp | 100 | 105 | 110 |     |
| gag gtg gtt agc gac acc gcc gag gcg ccg aag tca gcc gag gag cag |     |     |     | 384 |
| Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Gln | 115 | 120 | 125 |     |
| gcg gcc gaa tcg gcc aag ccg cac aag gtc aag cac cgc acg ttc cac |     |     |     | 432 |
| Ala Ala Glu Ser Ala Lys Pro His Lys Val Lys His Arg Thr Phe His | 130 | 135 | 140 |     |
| tac ccg ggt ggg ttg gtg gat ttc gtc aag cac atc aat cgc acc aaa |     |     |     | 480 |
| Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys | 145 | 150 | 155 | 160 |
| aac ccg atc cag cag agc gtc atc gac ttc gac ggc aaa gga acc ggg |     |     |     | 528 |
| Asn Pro Ile Gln Gln Ser Val Ile Asp Phe Asp Gly Lys Gly Thr Gly | 165 | 170 | 175 |     |
| cac gaa gtc gag atc gcg atg cag tgg aac ggt ggt tat tcg gag tcg |     |     |     | 576 |
| His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser | 180 | 185 | 190 |     |
| gtg cac acc ttc gcc aac acc atc aac acc cat gag ggc ggc acc cac |     |     |     | 624 |
| Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His | 195 | 200 | 205 |     |
| gag gag ggc ttc cgc agc gcg ctg acc tcg gtg gtg aac aag tac gcc |     |     |     | 672 |
| Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala | 210 | 215 | 220 |     |
| aaa gac aag aag ctg ctc aag gac aag gat ccc aac ctc acc ggc gac |     |     |     | 720 |
| Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp | 225 | 230 | 235 | 240 |
| gac atc cga gaa ggg ctg gcc gcg gtg atc tcc gtg aag gtc gcc gag |     |     |     | 768 |
| Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu | 245 | 250 | 255 |     |
| ccg cag ttc gag ggc cag act aag acg aaa ctc ggc aac acc gag gtc |     |     |     | 816 |
| Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val | 260 | 265 | 270 |     |
| aag tcg ttt gtc cag aaa gtc tgt aac gaa caa ctc act cac tgg ttc |     |     |     | 864 |
| Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe | 275 | 280 | 285 |     |
| gag gcg aac ccg tcg gaa gct aaa acc gtt gta aac aag gcg gtt tcg |     |     |     | 912 |
| Glu Ala Asn Pro Ser Glu Ala Lys Thr Val Val Asn Lys Ala Val Ser | 290 | 295 | 300 |     |

tcg gcc cag gcc cgc att gcg gcg cgt aag gcg cgg gag ttg gtg cgg 960  
 Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg  
 305 310 315 320

cgt aag agt gct acg gat ttg ggt ggg ttg ccg ggc aag ttg gct gat 1008  
 Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp  
 325 330 335

tgc cgc tcg acg gat ccg cgg aag tct gag ctg tat gtg gtg gaa ggt 1056  
 Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly  
 340 345 350

gat tcc gcg ggt ggg tcg gcg aaa agt ggg cgt gat tcg atg ttc cag 1104  
 Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln  
 355 360 365

gcg atc ttg ccg ctg cgc ggc aag atc atc aac gtc gaa aag gcc cgc 1152  
 Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg  
 370 375 380

atc gat cgg gtg ctg aaa aac acc gaa gtc cag gcc atc atc acc gcg 1200  
 Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala  
 385 390 395 400

ctg ggc acc ggc atc cac gac gaa ttc gac atc acc aaa ctg cgt tac 1248  
 Leu Gly Thr Gly Ile His Asp Glu Phe Asp Ile Thr Lys Leu Arg Tyr  
 405 410 415

cac aag atc gtg ttg 1263  
 His Lys Ile Val Leu  
 420

<210> 4

<211> 421

<212> PRT

<213> *Mycobacterium simiae*

<400> 4

Gly Glu Asn Ser Gly Tyr Thr Val Ser Gly Gly Leu His Gly Val Gly  
 1 5 10 15  
 Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asn Val Lys  
 20 25 30  
 Arg Asp Gly Tyr Glu Trp Phe Gln Tyr Tyr Asp Arg Ala Val Pro Gly  
 35 40 45  
 Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg  
 50 55 60  
 Phe Trp Ala Asp Pro Glu Ile Phe Glu Thr Thr Gln Tyr Asp Phe Glu  
 65 70 75 80  
 Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu  
 85 90 95  
 Thr Ile Asn Leu Thr Asp Glu Arg Val Glu Gln Asp Glu Val Val Asp  
 100 105 110  
 Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Gln  
 115 120 125  
 Ala Ala Glu Ser Ala Lys Pro His Lys Val Lys His Arg Thr Phe His  
 130 135 140

Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys  
 145 150 155 160  
 Asn Pro Ile Gln Gln Ser Val Ile Asp Phe Asp Gly Lys Gly Thr Gly  
 165 170 175  
 His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser  
 180 185 190  
 Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His  
 195 200 205  
 Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala  
 210 215 220  
 Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp  
 225 230 235 240  
 Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu  
 245 250 255  
 Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val  
 260 265 270  
 Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe  
 275 280 285  
 Glu Ala Asn Pro Ser Glu Ala Lys Thr Val Val Asn Lys Ala Val Ser  
 290 295 300  
 Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg  
 305 310 315 320  
 Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp  
 325 330 335  
 Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly  
 340 345 350  
 Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln  
 355 360 365  
 Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg  
 370 375 380  
 Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala  
 385 390 395 400  
 Leu Gly Thr Gly Ile His Asp Glu Phe Asp Ile Thr Lys Leu Arg Tyr  
 405 410 415  
 His Lys Ile Val Leu  
 420

<210> 5

<211> 660

<212> DNA

<213> Chitinophaga pinensis

<220>

<221> CDS

<222> (1)...(660)

<400> 5

gta gca ggc ttc cgc cgt gcg ata acc cgt atc ttc aag agc tat ggt 48  
 Val Ala Gly Phe Arg Arg Ala Ile Thr Arg Ile Phe Lys Ser Tyr Gly  
 1 5 10 15

gat aag aac aaa atg ttc gaa aaa acc aag atc gaa gta aca ggt gat 96  
 Asp Lys Asn Lys Met Phe Glu Lys Thr Lys Ile Glu Val Thr Gly Asp  
 20 25 30

gac ttc cgt gaa ggt ctg agc gct atc atc agc gta aaa gta cct gaa 144  
 Asp Phe Arg Glu Gly Leu Ser Ala Ile Ile Ser Val Lys Val Pro Glu

| 35  | 40  | 45  |     |
|---|-----|-----|-----|
| cca cag ttc gaa ggc cag acc aaa acc aaa ctc ggt aac tcc gat gta |     |     | 192 |
| Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Ser Asp Val |     |     |     |
| 50  | 55  | 60  |     |
| atg ggg gtt gtg gac agt tcc gta gca gcc gta ctg gat gcc tac ctg |     |     | 240 |
| Met Gly Val Val Asp Ser Ser Val Ala Ala Val Leu Asp Ala Tyr Leu |     |     |     |
| 65  | 70  | 75  | 80  |
| gaa gaa cat ccc cgc gaa gcc aag atc att atc aat aaa gtg gta ctg |     |     | 288 |
| Glu Glu His Pro Arg Glu Ala Lys Ile Ile Ile Asn Lys Val Val Leu |     |     |     |
|   | 85  | 90  | 95  |
| gca gca cag gcg cgt gaa gca gcc cgt aaa gca cgc cag atg gta cag |     |     | 336 |
| Ala Ala Gln Ala Arg Glu Ala Ala Arg Lys Ala Arg Gln Met Val Gln |     |     |     |
|   | 100 | 105 | 110 |
| cgt aag agc gta ctg agt gga agc ggc ttg oct ggt aaa ctg gct gac |     |     | 384 |
| Arg Lys Ser Val Leu Ser Gly Ser Gly Leu Pro Gly Lys Leu Ala Asp |     |     |     |
|   | 115 | 120 | 125 |
| tgc tct gaa aat gat cct gaa aaa tgt gaa ctg tac ctg gta gag ggt |     |     | 432 |
| Cys Ser Glu Asn Asp Pro Glu Lys Cys Glu Leu Tyr Leu Val Glu Gly |     |     |     |
|   | 130 | 135 | 140 |
| gac tcc gca ggt ggt acg gct aaa caa gga cgt aac cgt agc ttc cag |     |     | 480 |
| Asp Ser Ala Gly Gly Thr Ala Lys Gln Gly Arg Asn Arg Ser Phe Gln |     |     |     |
|   | 145 | 150 | 155 |
| gcg atc ctg ccg ctc agg ggt aaa atc ctg aac gtg gag aaa gcc atg |     |     | 528 |
| Ala Ile Leu Pro Leu Arg Gly Lys Ile Leu Asn Val Glu Lys Ala Met |     |     |     |
|   | 165 | 170 | 175 |
| gag cat aag ata tat gag aat gag gag att aaa aac atc ttc acc gca |     |     | 576 |
| Glu His Lys Ile Tyr Glu Asn Glu Glu Ile Lys Asn Ile Phe Thr Ala |     |     |     |
|   | 180 | 185 | 190 |
| ctt ggt gta acc atc ggt acg gaa gaa gat gac aaa gcc ctc aac ctc |     |     | 624 |
| Leu Gly Val Thr Ile Gly Thr Glu Glu Asp Asp Lys Ala Leu Asn Leu |     |     |     |
|   | 195 | 200 | 205 |
| tcc aaa ctg cgc tat cac aaa ctg atc atc atg acg                 |     |     | 660 |
| Ser Lys Leu Arg Tyr His Lys Leu Ile Ile Met Thr                 |     |     |     |
|   | 210 | 215 | 220 |
| <210> 6   |     |     |     |
| <211> 220   |     |     |     |
| <212> PRT   |     |     |     |
| <213> Chitinophaga pinensis                                     |     |     |     |
| <400> 6   |     |     |     |
| Val Ala Gly Phe Arg Arg Ala Ile Thr Arg Ile Phe Lys Ser Tyr Gly |     |     |     |
| 1   | 5   | 10  | 15  |
| Asp Lys Asn Lys Met Phe Glu Lys Thr Lys Ile Glu Val Thr Gly Asp |     |     |     |
|   | 20  | 25  | 30  |
| Asp Phe Arg Glu Gly Leu Ser Ala Ile Ile Ser Val Lys Val Pro Glu |     |     |     |





att aca atc aca ctt aca gat aaa aga cat act aaa gac aac ggc gat 336  
 Ile Thr Ile Thr Leu Thr Asp Lys Arg His Thr Lys Asp Asn Gly Asp  
                   100                  105                  110

ttt gaa ggt gaa gtt ttt cat tct aaa gaa ggg ctt aaa gaa ttc gtt 384  
 Phe Glu Gly Glu Val Phe His Ser Lys Glu Gly Leu Lys Glu Phe Val  
                   115                  120                  125

cga ttt tta gat gct ggt aga gaa cca att att tct cac gta ata agc 432  
 Arg Phe Leu Asp Ala Gly Arg Glu Pro Ile Ile Ser His Val Ile Ser  
                   130                  135                  140

atg gag cac gaa aaa gga gaa gtt cct gtt gag gtt gct ctt gtt tac 480  
 Met Glu His Glu Lys Gly Glu Val Pro Val Glu Val Ala Leu Val Tyr  
                   145                  150                  155                  160

aat aca agt tac tcc gaa aat att ttc tct tac gta aat aat att aac 528  
 Asn Thr Ser Tyr Ser Glu Asn Ile Phe Ser Tyr Val Asn Asn Ile Asn  
                   165                  170                  175

acg cac gaa 537  
 Thr His Glu

&lt;210&gt; 8

&lt;211&gt; 179

&lt;212&gt; PRT

&lt;213&gt; Flavobacterium aquatile

&lt;400&gt; 8

Asp Lys Asp Ser Tyr Lys Val Ser Gly Gly Leu His Gly Val Gly Val  
   1                  5                  10                  15

Ser Cys Val Asn Ala Leu Ser Asp Asn Leu Lys Ala Thr Val Phe Arg  
                   20                  25                  30

Asp Gly Lys Val Tyr Glu Gln Glu Tyr Glu Lys Gly Lys Ala Met Tyr  
                   35                  40                  45

Pro Val Lys Gln Val Gly Glu Thr Thr Lys Arg Gly Thr Met Val Thr  
                   50                  55                  60

Phe His Pro Asp Lys Thr Ile Phe Thr Gln Thr Ile Glu Tyr Ser Tyr  
                   65                  70                  75                  80

Asp Thr Leu Ala Ala Arg Met Arg Glu Leu Ser Phe Leu Asn Lys Gly  
                   85                  90                  95

Ile Thr Ile Thr Leu Thr Asp Lys Arg His Thr Lys Asp Asn Gly Asp  
                   100                  105                  110

Phe Glu Gly Glu Val Phe His Ser Lys Glu Gly Leu Lys Glu Phe Val  
                   115                  120                  125

Arg Phe Leu Asp Ala Gly Arg Glu Pro Ile Ile Ser His Val Ile Ser  
                   130                  135                  140

Met Glu His Glu Lys Gly Glu Val Pro Val Glu Val Ala Leu Val Tyr  
                   145                  150                  155                  160

Asn Thr Ser Tyr Ser Glu Asn Ile Phe Ser Tyr Val Asn Asn Ile Asn  
                   165                  170                  175

Thr His Glu

&lt;210&gt; 9

<211> 783  
 <212> DNA  
 <213> Mycobacterium asiaticum

<220>  
 <221> CDS  
 <222> (1)...(783)

<400> 9

|   |     |
|---|-----|
| ggc gag aac agc ggc tac acc gtc agc ggt ggg ttg cac gga gtg ggc | 48  |
| Gly Glu Asn Ser Gly Tyr Thr Val Ser Gly Gly Leu His Gly Val Gly |     |
| 1 5 10 15   |     |
| gtg tcg gtg gtc aac gcg ctg tcc acc cgc ctg gag gtc acc atc aag | 96  |
| Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Thr Ile Lys |     |
| 20 25 30  |     |
| cgc gac ggg cac gag tgg ttt cag tac tac gac cgc gcc gtg ccc gga | 144 |
| Arg Asp Gly His Glu Trp Phe Gln Tyr Tyr Asp Arg Ala Val Pro Gly |     |
| 35 40 45  |     |
| acc ctc aag cag ggc gag gcc acc aag aag acc gga acc acg atc agg | 192 |
| Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg |     |
| 50 55 60  |     |
| ttc tgg gcg gac ccc gaa atc ttc gaa acc aca cag tac gac ttc gag | 240 |
| Phe Trp Ala Asp Pro Glu Ile Phe Glu Thr Thr Gln Tyr Asp Phe Glu |     |
| 65 70 75 80   |     |
| acc gtg gcg cgg cgg ctg cag gag atg gcc ttc ctc aac aag ggc ctc | 288 |
| Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu |     |
| 85 90 95  |     |
| acc atc aac ctc acc gac gaa cga gtg gag cag gac gag gtc gtc gac | 336 |
| Thr Ile Asn Leu Thr Asp Glu Arg Val Glu Gln Asp Glu Val Val Asp |     |
| 100 105 110   |     |
| gag gtc gtc agc gac acc gcc gag gca ccg aag tcc gcc gaa gag aag | 384 |
| Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Lys |     |
| 115 120 125   |     |
| gcc gcg gaa tcg act gcg cca cac aag gtc aag cac cgc acc ttc cac | 432 |
| Ala Ala Glu Ser Thr Ala Pro His Lys Val Lys His Arg Thr Phe His |     |
| 130 135 140   |     |
| tac ccc ggc ggt ctg gtc gac ttc gtc aag cac atc aac cgc acc aag | 480 |
| Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys |     |
| 145 150 155 160   |     |
| agc ccg atc cag cag agc gtc atc gat ttc gac ggc aag ggc acc ggc | 528 |
| Ser Pro Ile Gln Gln Ser Val Ile Asp Phe Asp Gly Lys Gly Thr Gly |     |
| 165 170 175   |     |
| cac gag gtc gag atc gcc atg cag tgg aac ggc ggc tac tcg gag tcc | 576 |
| His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser |     |
| 180 185 190   |     |

gtc cac acc ttc gcc aac acc atc aac acg cac gag ggc ggc acc cac 624  
 Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His  
           195                          200                          205  
  
 gag gag ggc ttc cgc agc gcg ctg acg tcg gtg gtg aac aag tac gcc 672  
 Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala  
           210                          215                          220  
  
 aaa gac aag aaa ctg ctg aag gac aaa gat ccc aac ctc acc ggt gac 720  
 Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp  
           225                          230                          235                          240  
  
 gac atc cgt gag ggc ttg gcc gcg gtc atc tcg gtg aag gtc gcc gag 768  
 Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu  
                           245                          250                          255  
  
 cca cag ttc gaa ggc 783  
 Pro Gln Phe Glu Gly  
                           260

<210> 10

<211> 261

<212> PRT

<213> Mycobacterium asiaticum

<400> 10

Gly Glu Asn Ser Gly Tyr Thr Val Ser Gly Gly Leu His Gly Val Gly  
   1                          5                          10                          15  
 Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Thr Ile Lys  
                           20                          25                          30  
 Arg Asp Gly His Glu Trp Phe Gln Tyr Tyr Asp Arg Ala Val Pro Gly  
           35                          40                          45  
 Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg  
   50                          55                          60  
 Phe Trp Ala Asp Pro Glu Ile Phe Glu Thr Thr Gln Tyr Asp Phe Glu  
   65                          70                          75                          80  
 Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu  
                           85                          90                          95  
 Thr Ile Asn Leu Thr Asp Glu Arg Val Glu Gln Asp Glu Val Val Asp  
                           100                          105                          110  
 Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Lys  
           115                          120                          125  
 Ala Ala Glu Ser Thr Ala Pro His Lys Val Lys His Arg Thr Phe His  
   130                          135                          140  
 Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys  
 145                          150                          155                          160  
 Ser Pro Ile Gln Gln Ser Val Ile Asp Phe Asp Gly Lys Gly Thr Gly  
                           165                          170                          175  
 His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser  
                           180                          185                          190  
 Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His  
           195                          200                          205  
 Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala  
   210                          215                          220  
 Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp  
 225                          230                          235                          240  
 Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu

Pro Gln Phe Glu Gly      245      250      255  
                          260

<210> 11  
 <211> 195  
 <212> DNA  
 <213> Cytophaga lytica

<220>  
 <221> CDS  
 <222> (1)...(195)

<400> 11  
 agc cac att gaa act tta att ctt aca ttc ttc ttc cgt ttt atg cga      48  
 Ser His Ile Glu Thr Leu Ile Leu Thr Phe Phe Phe Arg Phe Met Arg  
      1                       5                       10                       15  
 gaa cta ata gaa ggc gga cac gtt tac ata gca aca cca cct tta tat      96  
 Glu Leu Ile Glu Gly Gly His Val Tyr Ile Ala Thr Pro Pro Leu Tyr  
                          20                       25                       30  
 tta gtt aaa aaa gga act aaa aag cgt tat gct tgg aat gat aaa gaa      144  
 Leu Val Lys Lys Gly Thr Lys Lys Arg Tyr Ala Trp Asn Asp Lys Glu  
                          35                       40                       45  
 cga gat gaa ata gca gat agc ttt aat ggt agt gta ggt atc caa aga      192  
 Arg Asp Glu Ile Ala Asp Ser Phe Asn Gly Ser Val Gly Ile Gln Arg  
      50                       55                       60  
 tat      195  
 Tyr  
      65

<210> 12  
 <211> 65  
 <212> PRT  
 <213> Cytophaga lytica

<400> 12  
 Ser His Ile Glu Thr Leu Ile Leu Thr Phe Phe Phe Arg Phe Met Arg  
      1                       5                       10                       15  
 Glu Leu Ile Glu Gly Gly His Val Tyr Ile Ala Thr Pro Pro Leu Tyr  
                          20                       25                       30  
 Leu Val Lys Lys Gly Thr Lys Lys Arg Tyr Ala Trp Asn Asp Lys Glu  
                          35                       40                       45  
 Arg Asp Glu Ile Ala Asp Ser Phe Asn Gly Ser Val Gly Ile Gln Arg  
      50                       55                       60  
 Tyr  
      65

<210> 13  
 <211> 1170  
 <212> DNA  
 <213> Synechococcus sp.

<220>

&lt;221&gt; CDS

&lt;222&gt; (1)...(1170)

&lt;400&gt; 13

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gtg | gtg | gac | aac | gcc | gtc | gac | aaa | gcc | ttg | gcg | ggc | tac | tgc | aat | acc | 48  |
| Val | Val | Asp | Asn | Ala | Val | Asp | Lys | Ala | Leu | Ala | Gly | Tyr | Cys | Asn | Thr |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| att | gat | gtt | cgt | ctg | ctc | aaa | gac | ggc | tcc | tgc | caa | gtc | acc | gat | aac | 96  |
| Ile | Asp | Val | Arg | Leu | Leu | Lys | Asp | Gly | Ser | Cys | Gln | Val | Thr | Asp | Asn |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| ggt | cgc | ggc | att | ccc | aca | gat | att | cac | ccc | caa | acc | ggg | aag | tct | gct | 144 |
| Gly | Arg | Gly | Ile | Pro | Thr | Asp | Ile | His | Pro | Gln | Thr | Gly | Lys | Ser | Ala |     |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| ctc | gaa | acc | gtg | ctg | acg | att | ctg | cac | gcg | ggc | ggc | aag | ttt | ggc | ggt | 192 |
| Leu | Glu | Thr | Val | Leu | Thr | Ile | Leu | His | Ala | Gly | Gly | Lys | Phe | Gly | Gly |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| ggc | ggt | tat | aag | gtg | tgc | ggg | ggt | ctg | cac | ggc | gtc | ggt | gtg | tct | gtc | 240 |
| Gly | Gly | Tyr | Lys | Val | Ser | Gly | Gly | Leu | His | Gly | Val | Gly | Val | Ser | Val |     |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |     |
| gtc | aac | gcc | ctc | tca | gaa | tat | gtc | gaa | gtc | acc | gtg | tgg | cgg | gaa | ggc | 288 |
| Val | Asn | Ala | Leu | Ser | Glu | Tyr | Val | Glu | Val | Thr | Val | Trp | Arg | Glu | Gly |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| aaa | acc | cac | caa | cag | cgc | ttt | gaa | cag | ggc | aac | ccg | atc | ggg | gag | ttg | 336 |
| Lys | Thr | His | Gln | Gln | Arg | Phe | Glu | Gln | Gly | Asn | Pro | Ile | Gly | Glu | Leu |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| caa | gtt | gcc | ccg | gat | gcc | gac | gat | cgc | cgc | ggg | aca | caa | gtt | cgt | ttc | 384 |
| Gln | Val | Ala | Pro | Asp | Ala | Asp | Asp | Arg | Arg | Gly | Thr | Gln | Val | Arg | Phe |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| aaa | cca | gac | gcc | acg | atc | ttt | tct | gaa | aca | acc | gag | ttc | gat | tac | ggc | 432 |
| Lys | Pro | Asp | Ala | Thr | Ile | Phe | Ser | Glu | Thr | Thr | Glu | Phe | Asp | Tyr | Gly |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| acc | cta | gca | agc | cga | ttg | aag | gag | cta | gcc | tat | ctg | aat | gcg | ggc | gtc | 480 |
| Thr | Leu | Ala | Ser | Arg | Leu | Lys | Glu | Leu | Ala | Tyr | Leu | Asn | Ala | Gly | Val |     |
|     | 145 |     |     |     | 150 |     |     |     | 155 |     |     |     |     | 160 |     |     |
| cgc | atc | gac | ttt | acc | gat | gag | cgg | ctg | cag | ctc | acc | aag | aat | cac | gag | 528 |
| Arg | Ile | Asp | Phe | Thr | Asp | Glu | Arg | Leu | Gln | Leu | Thr | Lys | Asn | His | Glu |     |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |     |
| ccc | cat | caa | gaa | acc | tat | tac | ttt | gaa | ggc | ggt | att | cgc | gaa | tac | gtc | 576 |
| Pro | His | Gln | Glu | Thr | Tyr | Tyr | Phe | Glu | Gly | Gly | Ile | Arg | Glu | Tyr | Val |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| gcc | tac | atg | aat | acc | gat | aaa | cag | gcg | ctg | cac | tca | gag | att | atc | ttt | 624 |
| Ala | Tyr | Met | Asn | Thr | Asp | Lys | Gln | Ala | Leu | His | Ser | Glu | Ile | Ile | Phe |     |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |     |
| gtg | caa | tcc | gaa | aaa | gat | ggc | gtc | caa | gtt | gaa | gct | gca | ttg | caa | tgg | 672 |

Val Gln Ser Glu Lys Asp Gly Val Gln Val Glu Ala Ala Leu Gln Trp  
 210 215 220

tgc gtt gac gcc tac agc gac aac att ctg ggc ttt gcc aac aac atc 720  
 Cys Val Asp Ala Tyr Ser Asp Asn Ile Leu Gly Phe Ala Asn Asn Ile  
 225 230 235 240

cgc acg att gac ggc ggc acc cat att gag ggc ctc aaa act gtt ctg 768  
 Arg Thr Ile Asp Gly Gly Thr His Ile Glu Gly Leu Lys Thr Val Leu  
 245 250 255

acg cgg acg atg aac acg atc gcc cgc aaa cgg aat aaa cgc aag gat 816  
 Thr Arg Thr Met Asn Thr Ile Ala Arg Lys Arg Asn Lys Arg Lys Asp  
 260 265 270

gcc gac aat aac ctg tcg ggc gag aat att cgc gaa ggc tta aca gcg 864  
 Ala Asp Asn Asn Leu Ser Gly Glu Asn Ile Arg Glu Gly Leu Thr Ala  
 275 280 285

atc gtt tcg gtc aaa gtt ccg gat ccg gaa ttt gaa ggc caa acc aaa 912  
 Ile Val Ser Val Lys Val Pro Asp Pro Glu Phe Glu Gly Gln Thr Lys  
 290 295 300

aca aag ctc ggc aat acc gaa gtt cgc ggc atc gtc gat acg ctc gtg 960  
 Thr Lys Leu Gly Asn Thr Glu Val Arg Gly Ile Val Asp Thr Leu Val  
 305 310 315 320

ggc gaa acg ttg acg gaa tat ctg gaa ttc cat ccc agc gtt gcc gat 1008  
 Gly Glu Thr Leu Thr Glu Tyr Leu Glu Phe His Pro Ser Val Ala Asp  
 325 330 335

ttg atc ctc gaa aaa gcg att caa gcc ttt aat gcg gct gag gca gcg 1056  
 Leu Ile Leu Glu Lys Ala Ile Gln Ala Phe Asn Ala Ala Glu Ala Ala  
 340 345 350

cga cgg gca cgg gaa ttg gtg cgt cgc aaa tca gtg ctg gaa tct tcg 1104  
 Arg Arg Ala Arg Glu Leu Val Arg Arg Lys Ser Val Leu Glu Ser Ser  
 355 360 365

aca ttg ccc ggt aaa tta gca gac tgt tcc agt cgc gat ccc ggt gaa 1152  
 Thr Leu Pro Gly Lys Leu Ala Asp Cys Ser Ser Arg Asp Pro Gly Glu  
 370 375 380

tct gaa atc ttc atc gtg 1170  
 Ser Glu Ile Phe Ile Val  
 385 390

<210> 14  
 <211> 390  
 <212> PRT  
 <213> Synechococcus sp.

<400> 14  
 Val Val Asp Asn Ala Val Asp Lys Ala Leu Ala Gly Tyr Cys Asn Thr  
 1 5 10 15  
 Ile Asp Val Arg Leu Leu Lys Asp Gly Ser Cys Gln Val Thr Asp Asn  
 20 25 30

Gly Arg Gly Ile Pro Thr Asp Ile His Pro Gln Thr Gly Lys Ser Ala  
           35                          40                          45  
 Leu Glu Thr Val Leu Thr Ile Leu His Ala Gly Gly Lys Phe Gly Gly  
           50                          55                          60  
 Gly Gly Tyr Lys Val Ser Gly Gly Leu His Gly Val Gly Val Ser Val  
           65                          70                          75                          80  
 Val Asn Ala Leu Ser Glu Tyr Val Glu Val Thr Val Trp Arg Glu Gly  
                           85                          90                          95  
 Lys Thr His Gln Arg Phe Glu Gln Gly Asn Pro Ile Gly Glu Leu  
                   100                          105                          110  
 Gln Val Ala Pro Asp Ala Asp Asp Arg Arg Gly Thr Gln Val Arg Phe  
           115                          120                          125  
 Lys Pro Asp Ala Thr Ile Phe Ser Glu Thr Thr Glu Phe Asp Tyr Gly  
           130                          135                          140  
 Thr Leu Ala Ser Arg Leu Lys Glu Leu Ala Tyr Leu Asn Ala Gly Val  
           145                          150                          155                          160  
 Arg Ile Asp Phe Thr Asp Glu Arg Leu Gln Leu Thr Lys Asn His Glu  
                           165                          170                          175  
 Pro His Gln Glu Thr Tyr Tyr Phe Glu Gly Gly Ile Arg Glu Tyr Val  
                   180                          185                          190  
 Ala Tyr Met Asn Thr Asp Lys Gln Ala Leu His Ser Glu Ile Ile Phe  
           195                          200                          205  
 Val Gln Ser Glu Lys Asp Gly Val Gln Val Glu Ala Ala Leu Gln Trp  
           210                          215                          220  
 Cys Val Asp Ala Tyr Ser Asp Asn Ile Leu Gly Phe Ala Asn Asn Ile  
           225                          230                          235                          240  
 Arg Thr Ile Asp Gly Gly Thr His Ile Glu Gly Leu Lys Thr Val Leu  
                           245                          250                          255  
 Thr Arg Thr Met Asn Thr Ile Ala Arg Lys Arg Asn Lys Arg Lys Asp  
                   260                          265                          270  
 Ala Asp Asn Asn Leu Ser Gly Glu Asn Ile Arg Glu Gly Leu Thr Ala  
           275                          280                          285  
 Ile Val Ser Val Lys Val Pro Asp Pro Glu Phe Glu Gly Gln Thr Lys  
           290                          295                          300  
 Thr Lys Leu Gly Asn Thr Glu Val Arg Gly Ile Val Asp Thr Leu Val  
           305                          310                          315                          320  
 Gly Glu Thr Leu Thr Glu Tyr Leu Glu Phe His Pro Ser Val Ala Asp  
                           325                          330                          335  
 Leu Ile Leu Glu Lys Ala Ile Gln Ala Phe Asn Ala Ala Glu Ala Ala  
           340                          345                          350  
 Arg Arg Ala Arg Glu Leu Val Arg Arg Lys Ser Val Leu Glu Ser Ser  
           355                          360                          365  
 Thr Leu Pro Gly Lys Leu Ala Asp Cys Ser Ser Arg Asp Pro Gly Glu  
           370                          375                          380  
 Ser Glu Ile Phe Ile Val  
           385                          390

&lt;210&gt; 15

&lt;211&gt; 696

&lt;212&gt; DNA

<213> *Caulobacter crescentus*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(696)

&lt;400&gt; 15



|   |     |
|---|-----|
| cag aac agc tac aag gtc tcg ggc ggt ctg cac ggc gtg ggc gtc tcg<br>Gln Asn Ser Tyr Lys Val Ser Gly Gly Leu His Gly Val Gly Val Ser<br>1 5 10 15       | 48  |
| gtc gtg aac gcc ctg tcg gat tgg ctg gag ctg ctg atc cac cgc aac<br>Val Val Asn Ala Leu Ser Asp Trp Leu Glu Leu Leu Ile His Arg Asn<br>20 25 30        | 96  |
| ggc aag gtc cac cag atg cgc ttc gag cgc ggc gac gcg gtc acc tcg<br>Gly Lys Val His Gln Met Arg Phe Glu Arg Gly Asp Ala Val Thr Ser<br>35 40 45        | 144 |
| ctg aag gtc acc ggc gac tcg ccc gtg cgg acc gag ggc ccc aag gcc<br>Leu Lys Val Thr Gly Asp Ser Pro Val Arg Thr Glu Gly Pro Lys Ala<br>50 55 60        | 192 |
| ggc gag acc ctg acc ggt acg gaa gtt acg ttc ttt ccg tcg aag gac<br>Gly Glu Thr Leu Thr Gly Thr Glu Val Thr Phe Phe Pro Ser Lys Asp<br>65 70 75 80     | 240 |
| acc ttc gcc ttc atc gaa ttc gac cgg aag acg ctg gag cac cgc ctg<br>Thr Phe Ala Phe Ile Glu Phe Asp Arg Lys Thr Leu Glu His Arg Leu<br>85 90 95        | 288 |
| cgc gag ctg gcc ttc ctg aac tcg ggc gtg acg atc tgg ttc aag gac<br>Arg Glu Leu Ala Phe Leu Asn Ser Gly Val Thr Ile Trp Phe Lys Asp<br>100 105 110     | 336 |
| cat cgc gac gtc gag ccg tgg gaa gag aag ctg ttc tac gag ggc ggc<br>His Arg Asp Val Glu Pro Trp Glu Glu Lys Leu Phe Tyr Glu Gly Gly<br>115 120 125     | 384 |
| atc gag gcc ttc gtg cgc cac ctc gac aag gcc aag acg ccg ctg ctg<br>Ile Glu Ala Phe Val Arg His Leu Asp Lys Ala Lys Thr Pro Leu Leu<br>130 135 140     | 432 |
| aag gcc ccg atc gcc gtc aag ggc gtc aag gac aag gtc gag atc gac<br>Lys Ala Pro Ile Ala Val Lys Gly Val Lys Asp Lys Val Glu Ile Asp<br>145 150 155 160 | 480 |
| ctg gcc ctg tgg tgg aac gac agc tac cac gag cag atg ctg tgc ttc<br>Leu Ala Leu Trp Trp Asn Asp Ser Tyr His Glu Gln Met Leu Cys Phe<br>165 170 175     | 528 |
| acc aac aac atc ccg cag ccg gat ggc ggc acg cac ctg tcg gcc ttt<br>Thr Asn Asn Ile Pro Gln Arg Asp Gly Gly Thr His Leu Ser Ala Phe<br>180 185 190     | 576 |
| cgc gcg gcc ctg acc ccg atc atc acc agc tac gcc gag agc tcc ggc<br>Arg Ala Ala Leu Thr Arg Ile Ile Thr Ser Tyr Ala Glu Ser Ser Gly<br>195 200 205     | 624 |
| atc ctg aag aag gaa aag gtc agc ctg ggc ggc gaa gac agc cgc gag<br>Ile Leu Lys Lys Glu Lys Val Ser Leu Gly Gly Glu Asp Ser Arg Glu<br>210 215 220     | 672 |
| ggc ctg acc tgc gtg ctg tcg gtc   | 696 |

Gly Leu Thr Cys Val Leu Ser Val  
225 230

<210> 16  
<211> 232  
<212> PRT  
<213> *Caulobacter crescentus*

<400> 16  
Gln Asn Ser Tyr Lys Val Ser Gly Gly Leu His Gly Val Gly Val Ser  
1 5 10 15  
Val Val Asn Ala Leu Ser Asp Trp Leu Glu Leu Leu Ile His Arg Asn  
20 25 30  
Gly Lys Val His Gln Met Arg Phe Glu Arg Gly Asp Ala Val Thr Ser  
35 40 45  
Leu Lys Val Thr Gly Asp Ser Pro Val Arg Thr Glu Gly Pro Lys Ala  
50 55 60  
Gly Glu Thr Leu Thr Gly Thr Glu Val Thr Phe Phe Pro Ser Lys Asp  
65 70 75 80  
Thr Phe Ala Phe Ile Glu Phe Asp Arg Lys Thr Leu Glu His Arg Leu  
85 90 95  
Arg Glu Leu Ala Phe Leu Asn Ser Gly Val Thr Ile Trp Phe Lys Asp  
100 105 110  
His Arg Asp Val Glu Pro Trp Glu Glu Lys Leu Phe Tyr Glu Gly Gly  
115 120 125  
Ile Glu Ala Phe Val Arg His Leu Asp Lys Ala Lys Thr Pro Leu Leu  
130 135 140  
Lys Ala Pro Ile Ala Val Lys Gly Val Lys Asp Lys Val Glu Ile Asp  
145 150 155 160  
Leu Ala Leu Trp Trp Asn Asp Ser Tyr His Glu Gln Met Leu Cys Phe  
165 170 175  
Thr Asn Asn Ile Pro Gln Arg Asp Gly Gly Thr His Leu Ser Ala Phe  
180 185 190  
Arg Ala Ala Leu Thr Arg Ile Ile Thr Ser Tyr Ala Glu Ser Ser Gly  
195 200 205  
Ile Leu Lys Lys Glu Lys Val Ser Leu Gly Gly Glu Asp Ser Arg Glu  
210 215 220  
Gly Leu Thr Cys Val Leu Ser Val  
225 230

<210> 17  
<211> 888  
<212> DNA  
<213> *Pseudomonas putida*

<220>  
<221> CDS  
<222> (1)...(888)

<400> 17  
ggc ggc ctg cac ggt gta ggc gtg tgc gta gtg aac gca ctg tct gaa 48  
Gly Gly Leu His Gly Val Gly Val Ser Val Val Asn Ala Leu Ser Glu  
1 5 10 15  
gag ctc gtc ctc acc gtt cgc cgt agc ggc aag atc tgg gaa cag acc 96  
Glu Leu Val Leu Thr Val Arg Arg Ser Gly Lys Ile Trp Glu Gln Thr  
20 25 30

|   |     |
|---|-----|
| tac gtc cat ggt gtt ccg cag gaa ccg atg aag atc gtt ggc gac agc<br>Tyr Val His Gly Val Pro Gln Glu Pro Met Lys Ile Val Gly Asp Ser<br>35 40 45        | 144 |
| gaa acc acc ggc acc cag atc cac ttc aag gct tcc agc gaa acc ttc<br>Glu Thr Thr Gly Thr Gln Ile His Phe Lys Ala Ser Ser Glu Thr Phe<br>50 55 60        | 192 |
| aag aac atc cac ttc agc tgg gac atc ctg gcc aag cgg att cgt gaa<br>Lys Asn Ile His Phe Ser Trp Asp Ile Leu Ala Lys Arg Ile Arg Glu<br>65 70 75 80     | 240 |
| ctg tcc ttc ctc aac tcc ggt gtc ggc atc gtc ctc aag gat gag cgc<br>Leu Ser Phe Leu Asn Ser Gly Val Gly Ile Val Leu Lys Asp Glu Arg<br>85 90 95        | 288 |
| agc ggc aag gaa gaa ctg ttc aag tac gaa ggc ggc ttg cgc gcg ttc<br>Ser Gly Lys Glu Glu Leu Phe Lys Tyr Glu Gly Gly Leu Arg Ala Phe<br>100 105 110     | 336 |
| gtt gaa tac ctg aac acc aac aag acc ccg gtc aac cag gtg ttc cat<br>Val Glu Tyr Leu Asn Thr Asn Lys Thr Pro Val Asn Gln Val Phe His<br>115 120 125     | 384 |
| ttc aac atc cag cgc gaa gac ggc atc ggc gta gaa atc gcc ctg cag<br>Phe Asn Ile Gln Arg Glu Asp Gly Ile Gly Val Glu Ile Ala Leu Gln<br>130 135 140     | 432 |
| tgg aac gac agc ttc aac gag aac ctg ttg tgc ttc acc aac aac att<br>Trp Asn Asp Ser Phe Asn Glu Asn Leu Leu Cys Phe Thr Asn Asn Ile<br>145 150 155 160 | 480 |
| ccg cag cgc gat ggc ggt act cac ctg gtg ggt ttc cgt tcc gcc ctg<br>Pro Gln Arg Asp Gly Gly Thr His Leu Val Gly Phe Arg Ser Ala Leu<br>165 170 175     | 528 |
| acg cgt aac ctc aat acg tat atc gaa gcc gaa ggc ctg gcg aag aag<br>Thr Arg Asn Leu Asn Thr Tyr Ile Glu Ala Glu Gly Leu Ala Lys Lys<br>180 185 190     | 576 |
| cac aag gtc gcg acc acc ggt gac gat gcc cgt gaa ggc ctg gcc gcg<br>His Lys Val Ala Thr Thr Gly Asp Asp Ala Arg Glu Gly Leu Ala Ala<br>195 200 205     | 624 |
| atc att tcg gta aaa gtg ccg gat ccg aag ttc agc tcc cag acc aag<br>Ile Ile Ser Val Lys Val Pro Asp Pro Lys Phe Ser Ser Gln Thr Lys<br>210 215 220     | 672 |
| gac aag ctg gtt tct tcc gaa gtg aag acc gcg gtc gaa cag gaa atg<br>Asp Lys Leu Val Ser Ser Glu Val Lys Thr Ala Val Glu Gln Glu Met<br>225 230 235 240 | 720 |
| ggc aag tac ttc tcc gac ttc ctg ctg gaa aac ccg aac gaa gcc aag<br>Gly Lys Tyr Phe Ser Asp Phe Leu Leu Glu Asn Pro Asn Glu Ala Lys<br>245 250 255     | 768 |

ctg gtt gtc ggc aag atg atc gac gcg gca cgt gct cgt gaa gcg gcg 816  
 Leu Val Val Gly Lys Met Ile Asp Ala Ala Arg Ala Arg Glu Ala Ala  
                   260                  265                  270

cgc aag acc cgt gag atg acc cgc cgc aaa ggc gcg ctg gac atc gcc 864  
 Arg Lys Thr Arg Glu Met Thr Arg Arg Lys Gly Ala Leu Asp Ile Ala  
                   275                  280                  285

ggc ctg ccg ggc aaa ctg gct gac 888  
 Gly Leu Pro Gly Lys Leu Ala Asp  
                   290                  295

<210> 18  
 <211> 296  
 <212> PRT  
 <213> Pseudomonas putida

<400> 18  
 Gly Gly Leu His Gly Val Gly Val Ser Val Val Asn Ala Leu Ser Glu  
   1                  5                  10                  15  
 Glu Leu Val Leu Thr Val Arg Arg Ser Gly Lys Ile Trp Glu Gln Thr  
                   20                  25                  30  
 Tyr Val His Gly Val Pro Gln Glu Pro Met Lys Ile Val Gly Asp Ser  
                   35                  40                  45  
 Glu Thr Thr Gly Thr Gln Ile His Phe Lys Ala Ser Ser Glu Thr Phe  
                   50                  55                  60  
 Lys Asn Ile His Phe Ser Trp Asp Ile Leu Ala Lys Arg Ile Arg Glu  
   65                  70                  75                  80  
 Leu Ser Phe Leu Asn Ser Gly Val Gly Ile Val Leu Lys Asp Glu Arg  
                   85                  90                  95  
 Ser Gly Lys Glu Glu Leu Phe Lys Tyr Glu Gly Gly Leu Arg Ala Phe  
                   100                  105                  110  
 Val Glu Tyr Leu Asn Thr Asn Lys Thr Pro Val Asn Gln Val Phe His  
                   115                  120                  125  
 Phe Asn Ile Gln Arg Glu Asp Gly Ile Gly Val Glu Ile Ala Leu Gln  
   130                  135                  140  
 Trp Asn Asp Ser Phe Asn Glu Asn Leu Leu Cys Phe Thr Asn Asn Ile  
  145                  150                  155                  160  
 Pro Gln Arg Asp Gly Gly Thr His Leu Val Gly Phe Arg Ser Ala Leu  
                   165                  170                  175  
 Thr Arg Asn Leu Asn Thr Tyr Ile Glu Ala Glu Gly Leu Ala Lys Lys  
                   180                  185                  190  
 His Lys Val Ala Thr Thr Gly Asp Asp Ala Arg Glu Gly Leu Ala Ala  
                   195                  200                  205  
 Ile Ile Ser Val Lys Val Pro Asp Pro Lys Phe Ser Ser Gln Thr Lys  
   210                  215                  220  
 Asp Lys Leu Val Ser Ser Glu Val Lys Thr Ala Val Glu Gln Glu Met  
  225                  230                  235                  240  
 Gly Lys Tyr Phe Ser Asp Phe Leu Leu Glu Asn Pro Asn Glu Ala Lys  
                   245                  250                  255  
 Leu Val Val Gly Lys Met Ile Asp Ala Ala Arg Ala Arg Glu Ala Ala  
                   260                  265                  270  
 Arg Lys Thr Arg Glu Met Thr Arg Arg Lys Gly Ala Leu Asp Ile Ala  
                   275                  280                  285  
 Gly Leu Pro Gly Lys Leu Ala Asp  
                   290                  295

<210> 19  
 <211> 531  
 <212> DNA  
 <213> Synechococcus sp.

<220>  
 <221> CDS  
 <222> (1)...(531)

<400> 19  
 ttg gtg cgt cgc aaa tca gtg ctg gaa tct tcg aca ttg ccc ggt aaa 48  
 Leu Val Arg Arg Lys Ser Val Leu Glu Ser Ser Thr Leu Pro Gly Lys  
 1 5 10 15

tta gca gac tgt tcc agt cgc gat ccc ggt gaa tct gaa atc ttc atc 96  
 Leu Ala Asp Cys Ser Ser Arg Asp Pro Gly Glu Ser Glu Ile Phe Ile  
 20 25 30

gtg gaa ggg gat tcg gca ggt ggc agt gct aaa cag ggg cgc gat cgc 144  
 Val Glu Gly Asp Ser Ala Gly Gly Ser Ala Lys Gln Gly Arg Asp Arg  
 35 40 45

cgc ttc caa gcc atc ctg cct ctg cgc ggc aaa atc ctc aac atc gag 192  
 Arg Phe Gln Ala Ile Leu Pro Leu Arg Gly Lys Ile Leu Asn Ile Glu  
 50 55 60

aaa acg gac gat gcc aaa atc tac aaa aac act gag atc caa gcc ctg 240  
 Lys Thr Asp Asp Ala Lys Ile Tyr Lys Asn Thr Glu Ile Gln Ala Leu  
 65 70 75 80

att aca gcg ctg ggc ctc gga att aaa ggg gag gaa ttt gat gct tcc 288  
 Ile Thr Ala Leu Gly Leu Gly Ile Lys Gly Glu Glu Phe Asp Ala Ser  
 85 90 95

caa ctg cgc tac cac cgt att gtg atc atg act gac gcg gac gtc gat 336  
 Gln Leu Arg Tyr His Arg Ile Val Ile Met Thr Asp Ala Asp Val Asp  
 100 105 110

ggt gcg cac atc cgt acc ctc ttg ctc acc ttc ttc tat cgc tat cag 384  
 Gly Ala His Ile Arg Thr Leu Leu Leu Thr Phe Phe Tyr Arg Tyr Gln  
 115 120 125

cga tcg ctg ctg gag cag ggc tac atg tac att gcc tgc ccg ccg ctg 432  
 Arg Ser Leu Leu Glu Gln Gly Tyr Met Tyr Ile Ala Cys Pro Pro Leu  
 130 135 140

tac aag ttg gag cgg gga cgt aat cac tac tat tgc tac aac gaa cgc 480  
 Tyr Lys Leu Glu Arg Gly Arg Asn His Tyr Tyr Cys Tyr Asn Glu Arg  
 145 150 155 160

gaa ctg cag gaa cgg att gcg acg ttc cct gaa aac gcc aac tat acg 528  
 Glu Leu Gln Glu Arg Ile Ala Thr Phe Pro Glu Asn Ala Asn Tyr Thr  
 165 170 175

att 531  
 Ile

<210> 20  
 <211> 177  
 <212> PRT  
 <213> *Synechococcus* sp.

<400> 20  
 Leu Val Arg Arg Lys Ser Val Leu Glu Ser Ser Thr Leu Pro Gly Lys  
   1                  5                  10                  15  
 Leu Ala Asp Cys Ser Ser Arg Asp Pro Gly Glu Ser Glu Ile Phe Ile  
                   20                  25                  30  
 Val Glu Gly Asp Ser Ala Gly Gly Ser Ala Lys Gln Gly Arg Asp Arg  
                   35                  40                  45  
 Arg Phe Gln Ala Ile Leu Pro Leu Arg Gly Lys Ile Leu Asn Ile Glu  
                   50                  55                  60  
 Lys Thr Asp Asp Ala Lys Ile Tyr Lys Asn Thr Glu Ile Gln Ala Leu  
                   65                  70                  75                  80  
 Ile Thr Ala Leu Gly Leu Gly Ile Lys Gly Glu Glu Phe Asp Ala Ser  
                   85                  90                  95  
 Gln Leu Arg Tyr His Arg Ile Val Ile Met Thr Asp Ala Asp Val Asp  
                   100                  105                  110  
 Gly Ala His Ile Arg Thr Leu Leu Leu Thr Phe Phe Tyr Arg Tyr Gln  
                   115                  120                  125  
 Arg Ser Leu Leu Glu Gln Gly Tyr Met Tyr Ile Ala Cys Pro Pro Leu  
                   130                  135                  140  
 Tyr Lys Leu Glu Arg Gly Arg Asn His Tyr Tyr Cys Tyr Asn Glu Arg  
                   145                  150                  155                  160  
 Glu Leu Gln Glu Arg Ile Ala Thr Phe Pro Glu Asn Ala Asn Tyr Thr  
                   165                  170                  175  
 Ile

<210> 21  
 <211> 660  
 <212> DNA  
 <213> *Caulobacter crescentus*

<220>  
 <221> CDS  
 <222> (1) ... (660)

<400> 21  
 cgg gat ggc ggc acg cac ctg tcg gcc ttt cgc gcg gcc ctg acc cgg 48  
 Arg Asp Gly Gly Thr His Leu Ser Ala Phe Arg Ala Ala Leu Thr Arg  
   1                  5                  10                  15  
 atc atc acc agc tac gcc gag agc tcc ggc atc ctg aag aag gaa aag 96  
 Ile Ile Thr Ser Tyr Ala Glu Ser Ser Gly Ile Leu Lys Lys Glu Lys  
                   20                  25                  30  
 gtc agc ctg ggc ggc gaa gac agc cgc gag ggc ctg acc tgc gtg ctg 144  
 Val Ser Leu Gly Gly Glu Asp Ser Arg Glu Gly Leu Thr Cys Val Leu  
                   35                  40                  45  
 tcg gtc aag gtc ccg gat ccg aag ttc agc tcg cag acc aag gac aag 192  
 Ser Val Lys Val Pro Asp Pro Lys Phe Ser Ser Gln Thr Lys Asp Lys  
                   50                  55                  60

ctg gtc tcg tcc gaa gtg cgc ccc gcc gtt gag ggc ctg gtg tcg gaa 240  
 Leu Val Ser Ser Glu Val Arg Pro Ala Val Glu Gly Leu Val Ser Glu  
 65 70 75 80  
 ggt ctc tcg acc tgg ttc gag gaa cat ccg aac gag gcc aag gcg atc 288  
 Gly Leu Ser Thr Trp Phe Glu Glu His Pro Asn Glu Ala Lys Ala Ile  
 85 90 95  
 gtg acc aag atc gcc gag gcc gcc gcc gcc cgc gag gcc gcc cgc aag 336  
 Val Thr Lys Ile Ala Glu Ala Ala Ala Ala Arg Glu Ala Ala Arg Lys  
 100 105 110  
 gcg cga gag ctg acc cgc cgc aag agc gcg ctc gac atc acc agc ctg 384  
 Ala Arg Glu Leu Thr Arg Arg Lys Ser Ala Leu Asp Ile Thr Ser Leu  
 115 120 125  
 ccc ggc aag ctc gcc gac tgc tcg gaa cgc gat ccg gcc aag tcc gag 432  
 Pro Gly Lys Leu Ala Asp Cys Ser Glu Arg Asp Pro Ala Lys Ser Glu  
 130 135 140  
 atc ttc atc gtc gag ggc gac tcg gcg ggc ggc tcg gcc aag cag gcc 480  
 Ile Phe Ile Val Glu Gly Asp Ser Ala Gly Gly Ser Ala Lys Gln Ala  
 145 150 155 160  
 cgc aac cgc gac aac cag gcc gtt ctg ccc ctg cgc ggc aag atc ctg 528  
 Arg Asn Arg Asp Asn Gln Ala Val Leu Pro Leu Arg Gly Lys Ile Leu  
 165 170 175  
 aac gtc gag cgg gcc cgc ttc gac aag atg ctg tcg tcc gac cag atc 576  
 Asn Val Glu Arg Ala Arg Phe Asp Lys Met Leu Ser Ser Asp Gln Ile  
 180 185 190  
 ggc acg ctg atc acc gcc ctg ggc gcg ggg atc ggc cgc gac gac ttc 624  
 Gly Thr Leu Ile Thr Ala Leu Gly Ala Gly Ile Gly Arg Asp Asp Phe  
 195 200 205  
 aac ccg gac aag gtg cgc tac cac aag atc gtg ctg 660  
 Asn Pro Asp Lys Val Arg Tyr His Lys Ile Val Leu  
 210 215 220

&lt;210&gt; 22

&lt;211&gt; 220

&lt;212&gt; PRT

<213> *Caulobacter crescentus*

&lt;400&gt; 22

Arg Asp Gly Gly Thr His Leu Ser Ala Phe Arg Ala Ala Leu Thr Arg  
 1 5 10 15  
 Ile Ile Thr Ser Tyr Ala Glu Ser Ser Gly Ile Leu Lys Lys Glu Lys  
 20 25 30  
 Val Ser Leu Gly Gly Glu Asp Ser Arg Glu Gly Leu Thr Cys Val Leu  
 35 40 45  
 Ser Val Lys Val Pro Asp Pro Lys Phe Ser Ser Gln Thr Lys Asp Lys  
 50 55 60  
 Leu Val Ser Ser Glu Val Arg Pro Ala Val Glu Gly Leu Val Ser Glu  
 65 70 75 80





|   |      |
|---|------|
| ttt tta tct gaa gtt ttt tac tct gaa gaa gga cta aaa gaa ttt att | 384  |
| Phe Leu Ser Glu Val Phe Tyr Ser Glu Glu Gly Leu Lys Glu Phe Ile |      |
| 115 120 125   |      |
| aag ttt tta gac ggt aac aga gaa caa cta ata cgt gat gtt gtt tca | 432  |
| Lys Phe Leu Asp Gly Asn Arg Glu Gln Leu Ile Arg Asp Val Val Ser |      |
| 130 135 140   |      |
| atg gaa ggt gaa aaa aac gga att cct gtt gag gtt gca atg gtg tac | 480  |
| Met Glu Gly Glu Lys Asn Gly Ile Pro Val Glu Val Ala Met Val Tyr |      |
| 145 150 155 160   |      |
| aat aca tca tat tca gaa aat ctt cac tct tac gta aat aat att aat | 528  |
| Asn Thr Ser Tyr Ser Glu Asn Leu His Ser Tyr Val Asn Asn Ile Asn |      |
| 165 170 175   |      |
| aca cat gaa ggt ggt aca cac ctt tca ggt ttt aga aga ggt tta aca | 576  |
| Thr His Glu Gly Gly Thr His Leu Ser Gly Phe Arg Arg Gly Leu Thr |      |
| 180 185 190   |      |
| tca acc tta aaa aag tat gca gat gca tct gga atg tta gac aaa tta | 624  |
| Ser Thr Leu Lys Lys Tyr Ala Asp Ala Ser Gly Met Leu Asp Lys Leu |      |
| 195 200 205   |      |
| aag ttt gag att cag gga gat gat ttt aga gaa ggt tta acg gct att | 672  |
| Lys Phe Glu Ile Gln Gly Asp Phe Arg Glu Gly Leu Thr Ala Ile     |      |
| 210 215 220   |      |
| gtg tct gtt aaa gtt gca gaa cct cag ttt gaa ggg caa aca aaa act | 720  |
| Val Ser Val Lys Val Ala Glu Pro Gln Phe Glu Gly Gln Thr Lys Thr |      |
| 225 230 235 240   |      |
| aaa tta ggt aac aga gaa gtt tct tct gca gtg agc caa gct gta tca | 768  |
| Lys Leu Gly Asn Arg Glu Val Ser Ser Ala Val Ser Gln Ala Val Ser |      |
| 245 250 255   |      |
| gaa atg ctt acc aac tat tta gaa gaa aac cca gat gat gct aag gta | 816  |
| Glu Met Leu Thr Asn Tyr Leu Glu Glu Asn Pro Asp Asp Ala Lys Val |      |
| 260 265 270   |      |
| att gta caa aaa gtc att ttg gca gcg caa gca cgt cat gcg gct aca | 864  |
| Ile Val Gln Lys Val Ile Leu Ala Ala Gln Ala Arg His Ala Ala Thr |      |
| 275 280 285   |      |
| aaa gcc cgt gaa atg gta cag cgt aaa acg gta atg agt ata ggt ggt | 912  |
| Lys Ala Arg Glu Met Val Gln Arg Lys Thr Val Met Ser Ile Gly Gly |      |
| 290 295 300   |      |
| tta cca ggg aaa tta tca gac tgt tct gag caa gat gct aca aaa tgc | 960  |
| Leu Pro Gly Lys Leu Ser Asp Cys Ser Glu Gln Asp Ala Thr Lys Cys |      |
| 305 310 315 320   |      |
| gaa gta ttc ctt gta gag gga gat tcg gcg ggt ggt act gct aaa caa | 1008 |
| Glu Val Phe Leu Val Glu Gly Asp Ser Ala Gly Gly Thr Ala Lys Gln |      |
| 325 330 335   |      |
| ggt agg gac aga aac ttt cag gca ata tta ccg ctt cgt ggt aaa atc | 1056 |

Gly Arg Asp Arg Asn Phe Gln Ala Ile Leu Pro Leu Arg Gly Lys Ile  
 340 345 350

tta aat gtt gaa aaa gca atg caa cat aag gtt ttt gaa aac gaa gaa 1104  
 Leu Asn Val Glu Lys Ala Met Gln His Lys Val Phe Glu Asn Glu Glu  
 355 360 365

ata aaa aat att tac aca gct tta ggt gtt act att ggt aca gaa gaa 1152  
 Ile Lys Asn Ile Tyr Thr Ala Leu Gly Val Thr Ile Gly Thr Glu Glu  
 370 375 380

gat agt aaa gcc tta aac tta gaa aaa tta aga tac cat aaa gta gtt 1200  
 Asp Ser Lys Ala Leu Asn Leu Glu Lys Leu Arg Tyr His Lys Val Val  
 385 390 395 400

att atg tgt gat gcc gat gta gat ggt agc cac att gaa act tta atc 1248  
 Ile Met Cys Asp Ala Asp Val Asp Gly Ser His Ile Glu Thr Leu Ile  
 405 410 415

ctt aca ttc ttc ttc cgt ttt atg agg gag tta ata gaa ggc ggt cac 1296  
 Leu Thr Phe Phe Phe Arg Phe Met Arg Glu Leu Ile Glu Gly Gly His  
 420 425 430

gtt tat ata gca acc cca cct tta tac ttg gta aaa aag gga aca aaa 1344  
 Val Tyr Ile Ala Thr Pro Pro Leu Tyr Leu Val Lys Lys Gly Thr Lys  
 435 440 445

aaa cgt tat gct tgg aat gat aaa gaa cga gat gag ata gca gaa agc 1392  
 Lys Arg Tyr Ala Trp Asn Asp Lys Glu Arg Asp Glu Ile Ala Glu Ser  
 450 455 460

ttt aat ggt agt gtt ggt ata caa aga tat 1422  
 Phe Asn Gly Ser Val Gly Ile Gln Arg Tyr  
 465 470

<210> 24

<211> 474

<212> PRT

<213> *Cytophaga lytica*

<400> 24

Asp Lys Asp Ser Tyr Lys Val Ser Gly Gly Leu His Gly Val Gly Val  
 1 5 10 15  
 Ser Cys Val Asn Ala Leu Ser Asn Asn Leu Lys Ala Thr Val Tyr Arg  
 20 25 30  
 Glu Gly Lys Ile Trp Glu Gln Glu Tyr Glu Arg Gly Lys Ala Leu Tyr  
 35 40 45  
 Pro Val Lys Ser Ile Gly Glu Thr Glu Glu Thr Gly Thr Ile Val Thr  
 50 55 60  
 Phe Tyr Pro Asp Asp Thr Ile Phe Thr Gln Thr Thr Glu Tyr Asn Tyr  
 65 70 75 80  
 Glu Thr Leu Ser Asn Arg Met Arg Glu Leu Ala Tyr Leu Asn Lys Gly  
 85 90 95  
 Val Thr Ile Ser Ile Thr Asp Lys Arg Val Lys Asp Glu Lys Gly Glu  
 100 105 110  
 Phe Leu Ser Glu Val Phe Tyr Ser Glu Glu Gly Leu Lys Glu Phe Ile  
 115 120 125

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Lys Phe Leu Asp Gly Asn Arg Glu Gln Leu Ile Arg Asp Val Val Ser
130                      135                      140
Met Glu Gly Glu Lys Asn Gly Ile Pro Val Glu Val Ala Met Val Tyr
145                      150                      155                      160
Asn Thr Ser Tyr Ser Glu Asn Leu His Ser Tyr Val Asn Asn Ile Asn
165                      170                      175
Thr His Glu Gly Gly Thr His Leu Ser Gly Phe Arg Arg Gly Leu Thr
180                      185                      190
Ser Thr Leu Lys Lys Tyr Ala Asp Ala Ser Gly Met Leu Asp Lys Leu
195                      200                      205
Lys Phe Glu Ile Gln Gly Asp Asp Phe Arg Glu Gly Leu Thr Ala Ile
210                      215                      220
Val Ser Val Lys Val Ala Glu Pro Gln Phe Glu Gly Gln Thr Lys Thr
225                      230                      235                      240
Lys Leu Gly Asn Arg Glu Val Ser Ser Ala Val Ser Gln Ala Val Ser
245                      250                      255
Glu Met Leu Thr Asn Tyr Leu Glu Glu Asn Pro Asp Asp Ala Lys Val
260                      265                      270
Ile Val Gln Lys Val Ile Leu Ala Ala Gln Ala Arg His Ala Ala Thr
275                      280                      285
Lys Ala Arg Glu Met Val Gln Arg Lys Thr Val Met Ser Ile Gly Gly
290                      295                      300
Leu Pro Gly Lys Leu Ser Asp Cys Ser Glu Gln Asp Ala Thr Lys Cys
305                      310                      315                      320
Glu Val Phe Leu Val Glu Gly Asp Ser Ala Gly Gly Thr Ala Lys Gln
325                      330                      335
Gly Arg Asp Arg Asn Phe Gln Ala Ile Leu Pro Leu Arg Gly Lys Ile
340                      345                      350
Leu Asn Val Glu Lys Ala Met Gln His Lys Val Phe Glu Asn Glu Glu
355                      360                      365
Ile Lys Asn Ile Tyr Thr Ala Leu Gly Val Thr Ile Gly Thr Glu Glu
370                      375                      380
Asp Ser Lys Ala Leu Asn Leu Glu Lys Leu Arg Tyr His Lys Val Val
385                      390                      395                      400
Ile Met Cys Asp Ala Asp Val Asp Gly Ser His Ile Glu Thr Leu Ile
405                      410                      415
Leu Thr Phe Phe Phe Arg Phe Met Arg Glu Leu Ile Glu Gly Gly His
420                      425                      430
Val Tyr Ile Ala Thr Pro Pro Leu Tyr Leu Val Lys Lys Gly Thr Lys
435                      440                      445
Lys Arg Tyr Ala Trp Asn Asp Lys Glu Arg Asp Glu Ile Ala Glu Ser
450                      455                      460
Phe Asn Gly Ser Val Gly Ile Gln Arg Tyr
465                      470

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<210> 25

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide for PCR

<221> misc\_feature

<222> 24, 27, 30

<223> n = A,T,C or G

<400> 25  
tgtaaaacga cggccagtca ygcngngngn aarttyga

38

<210> 26  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetically generated peptide

<400> 26  
His Ala Gly Gly Lys Phe Asp  
1 5

<210> 27  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide for PCR

<221> misc\_feature  
<222> 19, 25, 31  
<223> n = A,T,C or G

<400> 27  
ctgcgttcgt atatgagcnc crtcnacrtc ngcrtc

36

<210> 28  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthetically generated peptide

<400> 28  
Asp Ala Asp Val Asp Gly Ala His Ile Arg Thr Leu  
1 5 10

<210> 29  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
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<221> misc\_feature  
<222> 27, 30, 33  
<223> n = A,T,C or G

<400> 29  
gaagtcacga tgaccgttct gcaygsnggn ggnaarttyg g

41

<210> 30  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated peptide

<400> 30  
 Glu Val Leu Met Thr Val Leu His Ala Gly Gly Lys Phe Gly  
     1                    5                    10

<210> 31  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide for PCR

<221> misc\_feature  
 <222> 27, 33, 39  
 <223> n = A,T,C or G

<400> 31  
 agcagggtac ggatgtgcga gccrtcnacr tcngrtcng tgat

44

<210> 32  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated peptide

<400> 32  
 Met Thr Asp Ala Asp Val Asp Gly Ser His Ile Arg Thr Leu Leu  
     1                    5                    10                    15

<210> 33  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide for PCR

<221> misc\_feature  
 <222> 24, 27, 30  
 <223> n = A,T,C or G

<400> 33  
 caggaaacag ctatgaccar rtgngtnccn cc

32

<210> 34

<211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated peptide

<400> 34  
 Gly Gly Thr His Leu  
       1                  5

<210> 35  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide for PCR

<221> misc\_feature  
 <222> 20, 26, 29, 32  
 <223> n = A,T,C or G

<400> 35  
 gcaacgagat caacactcmn garggnggna cnca

34

<210> 36  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated peptide

<400> 36  
 Asn Asn Ile Asn Thr His Glu Gly Gly Thr His  
       1                  5                  10

<210> 37  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated peptide

<400> 37  
 Asn Asn Ile Asn Thr Pro Glu Gly Gly Thr His  
       1                  5                  10

<210> 38  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide for PCR

<221> misc\_feature  
 <222> 24, 30  
 <223> n = A,T,C or G

<400> 38  
 tgtaaaacga cggccagtar yttnkyyttt gtytg

35

<210> 39  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated peptide

<400> 39  
 Gln Thr Lys Thr Lys Leu  
     1                    5

<210> 40  
 <211> 6  
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<220>  
 <223> synthetically generated peptide

<400> 40  
 Gln Thr Lys Asp Lys Leu  
     1                    5

<210> 41  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide for PCR

<221> misc\_feature  
 <222> 24, 30  
 <223> n = A,T,C or G

<400> 41  
 taggctagct gaccgtaaga ygcngayrtn gaygg

35

<210> 42  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated peptide

<400> 42  
 Asp Ala Asp Val Asp Gly

1 5

<210> 43  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide for PCR

<221> misc\_feature  
 <222> 25, 28, 31  
 <223> n = A,T,C or G

<400> 43  
 ccatagctgc gtagcattca tytcnccnar nccytt 36

<210> 44  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated peptide

<400> 44  
 Lys Gly Leu Gly Glu Met Asn Ala Thr Gln Leu Trp  
 1 5 10

<210> 45  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide for PCR

<221> misc\_feature  
 <222> 24, 27, 30  
 <223> n = A,T,C or G

<400> 45  
 caggaaacag ctatgaccaa rmgnccngsn atgtayathg g 41

<210> 46  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated peptide

<400> 46  
 Lys Arg Pro Ala Met Tyr Ile Gly  
 1 5

<210> 47



<211> 8  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> synthetically generated peptide

<400> 47  
 Lys Arg Pro Gly Met Tyr Ile Gly  
     1                    5

<210> 48  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide for PCR

<221> misc\_feature  
 <222> 21, 24, 27, 33  
 <223> n = A,T,C or G

<400> 48  
 tgtaaaacga cggccagtcc nccngcnswr tcnccytc

38

<210> 49  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated peptide

<400> 49  
 Glu Gly Asp Ser Ala Gly Gly  
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<210> 50  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide for PCR

<221> misc\_feature  
 <222> 22, 25, 28, 34  
 <223> n = A,T,C or G

<400> 50  
 tgtaaaacga cggccagtca tngtngtntc ccanarytg

39

<210> 51  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> synthetically generated peptide

<400> 51

Gln Leu Trp Glu Thr Thr Met  
1 5

<210> 52

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated peptide

<400> 52

Gln Leu Trp Asp Thr Thr Met  
1 5

<210> 53

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide for PCR

<221> misc\_feature

<222> 27, 30, 33

<223> n = A,T,C or G

<400> 53

gaagtcacatca tgaccgttct gcaygcnggn ggnaarttyg a

41

<210> 54

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated peptide

<400> 54

Glu Val Ile Met Thr Val Leu His Ala Gly Gly Lys Phe Asp  
1 5 10

<210> 55

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated peptide

<400> 55

Glu Val Ile Met Thr Val Leu His Ala Gly Gly Lys Phe Asn

1                      5                      10  
 <210> 56  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> synthetically generated peptide  
  
 <400> 56  
 Glu Val Ile Met Thr Val Leu His Ala Gly Gly Lys Phe Glu  
   1                      5                      10  
  
 <210> 57  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> synthetically generated peptide  
  
 <400> 57  
 Glu Val Ile Met Thr Val Leu His Ala Gly Gly Lys Phe Lys  
   1                      5                      10  
  
 <210> 58  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> oligonucleotide for PCR  
  
 <221> misc\_feature  
 <222> 21  
 <223> n = A,T,C or G  
  
 <400> 58  
 tgtaaaacga cggccagtgc nggrtcytty tcytgrca  
  
 <210> 59  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> synthetically generated peptide  
  
 <400> 59  
 Cys Gln Glu Lys Asp Pro Ala  
   1                      5  
  
 <210> 60  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide for PCR  
  
 <221> misc\_feature  
 <222> 26, 38  
 <223> n = A,T,C or G  
  
 <400> 60  
 gaagtcatca tgaccgttct gcaacnaaya ayathccnca

40

<210> 61  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated peptide

<400> 61  
 Thr Asn Asn Ile Pro Gln  
 1 5

<210> 62  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide for PCR

<221> misc\_feature  
 <222> 24, 27, 30, 33  
 <223> n = A,T,C or G

<400> 62  
 tgtaaaacga cggccagtaa yttnggntcn ggnacytt

38

<210> 63  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated peptide

<400> 63  
 Lys Val Pro Asp Pro Lys Phe  
 1 5

<210> 64  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated peptide

<400> 64  
 Lys Val Pro Glu Pro Lys Phe  
     1                    5

<210> 65  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> oligonucleotide for PCR

<221> misc\_feature  
 <222> 21, 24, 27, 30, 33  
 <223> n = A,T,C or G

<400> 65  
 caggaaacag ctatgaccgc nmrmnrmngcn mgnga

35

<210> 66  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated peptide

<400> 66  
 Ala Arg Arg Ala Arg Glu  
     1                    5

<210> 67  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated peptide

<400> 67  
 Ala Arg Lys Ala Arg Glu  
     1                    5

<210> 68  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated peptide

<400> 68  
 Ala Lys Lys Ala Arg Glu  
     1                    5

<210> 69

<211> 19  
 <212> PRT  
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<220>  
 <223> synthetically generated peptide

<221> VARIANT  
 <222> 1  
 <223> Xaa = Pro or Ser

<221> VARIANT  
 <222> 2  
 <223> Xaa = Ala or Thr

<221> VARIANT  
 <222> 3  
 <223> Xaa = Ala, Val or Leu

<221> VARIANT  
 <222> 4  
 <223> Xaa = Glu or Asp

<221> VARIANT  
 <222> 5  
 <223> Xaa = Val or Thr

<221> VARIANT  
 <222> 6  
 <223> Xaa = Ile or Val

<221> VARIANT  
 <222> 7  
 <223> Xaa = Met, Leu or Phe

<221> VARIANT  
 <222> 9  
 <223> Xaa = Val, Gln or Ile

<221> VARIANT  
 <222> 17  
 <223> Xaa = Asp or Gly

<221> VARIANT  
 <222> 18  
 <223> Xaa = Asp, Gly, Asn or Ser

<221> VARIANT  
 <222> 19  
 <223> Xaa = Ser, Lys, Gly, Asp or Asn

<400> 69  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Xaa Leu His Ala Gly Gly Lys Phe  
   1                  5                  10                  15  
 Xaa Xaa Xaa

<210> 70  
 <211> 4  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated peptide

<400> 70  
 Gly Gly Thr His  
 1

<210> 71  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated peptide

<221> VARIANT  
 <222> 1  
 <223> Xaa = Ile or Leu

<221> VARIANT  
 <222> 10  
 <223> Xaa = Ala or Ser

<400> 71  
 Xaa Met Thr Asp Ala Asp Val Asp Gly Xaa His Ile Arg Thr Leu  
 1 5 10 15

<210> 72  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated peptide

<221> VARIANT  
 <222> 5  
 <223> Xaa = Gly or Ala

<221> VARIANT  
 <222> 10  
 <223> Xaa = Ser or Asp

<400> 72  
 Arg Lys Arg Pro Xaa Met Tyr Ile Gly Xaa Thr  
 1 5 10

<210> 73  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> synthetically generated peptide

<221> VARIANT

<222> 2

<223> Xaa = Thr or Pro

<221> VARIANT

<222> 3

<223> Xaa = Lys or Asn

<221> VARIANT

<222> 4

<223> Xaa = Thr, Asp, Gly, Lys, Ser, Phe or Tyr

<400> 73

Gln Xaa Xaa Xaa Lys Leu

1

5

<210> 74

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated peptide

<221> VARIANT

<222> 1

<223> Xaa = Tyr or Phe

<221> VARIANT

<222> 9

<223> Xaa = Ala or Pro

<400> 74

Xaa Lys Gly Leu Gly Glu Met Asn Xaa

1

5

<210> 75

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated peptide

<400> 75

Val Glu Gly Asp Ser Ala Gly Gly Ser

1

5

<210> 76

<211> 7

<212> PRT

<213> Artificial Sequence

<220>



<223> synthetically generated peptide

<221> VARIANT

<222> 2

<223> Xaa = His or Val

<221> VARIANT

<222> 6

<223> Xaa = Gln or Lys

<400> 76

Lys Xaa Pro Asp Pro Xaa Phe

1

5

<210> 77

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated peptide

<221> VARIANT

<222> 9

<223> Xaa = Ser or Gln

<221> VARIANT

<222> 10

<223> Xaa = Ser or Glu

<221> VARIANT

<222> 11

<223> Xaa = Lys or Arg

<221> VARIANT

<222> 14

<223> Xaa = Ala or Ser

<400> 77

Leu Pro Gly Lys Leu Ala Asp Cys Xaa Xaa Xaa Asp Pro Xaa

1

5

10

<210> 78

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated peptide

<221> VARIANT

<222> 3

<223> Xaa = Trp or Arg

<221> VARIANT

<222> 4

<223> Xaa = Glu or Asp

<221> VARIANT  
 <222> 7  
 <223> Xaa = Met or Leu

<221> VARIANT  
 <222> 8  
 <223> Xaa = Asp or Asn

<400> 78  
 Gln Leu Xaa Xaa Thr Thr Xaa Xaa Pro  
           1                          5

<210> 79  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated peptide

<221> VARIANT  
 <222> 2, 3  
 <223> Xaa = Lys or Arg

<400> 79  
 Ala Xaa Xaa Ala Arg Glu  
           1                          5

<210> 80  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated peptide

<221> VARIANT  
 <222> 6  
 <223> Xaa = Pro or Asn

<221> VARIANT  
 <222> 7  
 <223> Xaa = Thr or Gln

<400> 80  
 Phe Thr Asn Asn Ile Xaa Xaa  
           1                          5

<210> 81  
 <211> 7  
 <212> PRT  
 <213> Pseudomonas putida

<400> 81  
 His Ala Gly Gly Lys Phe Asp  
           1                          5

<210> 82

<211> 8

<212> PRT

<213> Pseudomonas putida

<400> 82

Met Thr Asp Ala Asp Val Asp Gly

1

5